

# SEQUENCE LISTING

<110> DSM IP Assets B.V.

<120> CARBOXYPEPTIDASE FOR CHEESE RIPENING

<130> 24178EP/P0/

<160> 3

<170> PatentIn version 3.1

<210> 1

<211> 1814

<212> DNA

<213> *Aspergillus niger*

<400> 1

atgcgggtta ccacggcaat tgcttcatta ctactggtcg gctcggccac cagtctccaa	60
aatcctcatc gtcgggtgtg tccgccctct ctctcgcatc gcagcgtagc gtctcgctcc	120
gtgcccgctg agcgcgcaac caccgacttt gagtatttga ctaacaagac tgcaagtgcg	180
tgattccgtt ttttaactac cgcatttate gttctaagat caattgcagg attcctggtc	240
aatggcacaa gcatcccgga agtcgatttc gacgtcggcg agtcctacgc cggcctcttc	300
cccaatacgc ccaactggcaa ttctagccta ttcttctggt tcttcccttc gcaaaatcca	360
gaggccacgc atgaggttag tggtcgctct gtttttccg gtcatgcgct agccagctaa	420
caattaacaa agatcaccat ctggctcaac ggcggcccg gatgtagctc cctagacggc	480
ctgcttcaag agaacggccc attcctctgg cagcctggca cttacaagcc cgttccctaat	540
ccatactcat ggaccaacct caccaatgtg gtttacatcg accaaccgcg cggcacaggc	600
ttctccccgg gccctcgcac cgtaaataac gaggaagacg tggctgcccc gttcaacagc	660
tggttcaagc acttcgtcga caccctcgac ctgcacggcc gcaaggtcta catcacgggt	720
gaaagctacg cgggcgtgta cgtccctcac attgccgatg ccatgctgaa cgaggaggat	780
acaacctact tcaacttgaa gggatatccg atcaacgacc cgtccatcaa cagcgactcg	840
gtcatgatgt actgtatggt tcccttcata tacctccacc tccaccacca ccaccactaa	900
caacatcacc caccagcccc cgcggtccgc catctgaacc actacaacaa catcttccag	960
ctaaactcca ctttctcttc ctacatcaac gccaaagccg acaagtcgcy ctacaacgcc	1020
ttctcgcaca aagccatcac ctaccacccc ccagtcctt tccccaccgc ccttgaatc	1080
accgaagact gccaaagtct ggacgaagtc gtcattggcc cctacgacat caaccctgc	1140
ttcaattact accacctgat cgacttctgc cctacctctt gggacgtgct cggcttcccc	1200

tcctctgctt cgggccccaa caactacttc aaccgctctg acgtccagaa gatctgcac	1260
gtccctccaa cggactactc cgtgtgctcg gagaccgtca tctctcgcaa cggcgacggc	1320
agcgacccca gctcctgggg tccctaccc agcgtcatcg aacgcactaa caacactatc	1380
atcggccacg gctggctcga ttacctcttc ttcttgaacg gctcgtctcg cacaatccag	1440
aacatgacct ggaacggtaa gcaagggttc cagcgtcttc cgtggaacc gctcttcgtc	1500
ccttaccatt atggctctgc tgagctgtac tggggcgatg agcctgaccc gtataacctt	1560
gatgctggcg ctggatacct gggtagacg cataccgagc gcgggttgac ttctagctcg	1620
gtgtatttgt ctggctatgg taagtttatt atatccctt ggaagcggta tgatgaacgt	1680
tagagagtgc tgaactgttc ttctctctcg tgatagaaat cccgcagtat gttctcggtg	1740
cggcttaccg ccagttggag ttctgtctcg gtaggattag tagtcttctg gcgaagggga	1800
actatacttc ttga	1814

<210> 2  
 <211> 1563  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 2	
atgcggttta ccacggcaat tgcttcatta ctactggtcg gctcggccac cagtctccaa	60
aatctctatc gtggggtgt tccgccccct ctctcgatc gcagcgtagc gtctcgctcc	120
gtgcccgttg agcgccgaac caccgacttt gagtatttga ctaacaagac tgcaagattc	180
ctgggtcaatg gcacaagcat ccccgaaatc gatttcgacg tcggcgagtc ctacgccggc	240
cttctcccca atacgccac tggcaattct agcctattct tctggttctt cccctcgcaa	300
aatccagagg ccagcgatga gatcaccatc tggctcaacg gcggccccgg atgtagctcc	360
ctagacggcc tgcctcaaga gaacggccca ttctctggc agcctggcac ttacaagccc	420
gttctctaate catactcatg gaccaacctc accaatgtgg ttatcatcga ccaaccggcc	480
ggcacaggct tctccccggg cccctcgacc gtaataaacg aggaagacgt ggctgccag	540
ttcaacagct ggttcaagca ctctgtcgac accttcgacc tgacggcgcc caaggtctac	600
atcacccggtg aaagctacgc gggcatgtac gtccccata ttgccgatgc catgctgaac	660
gaggaggata caactactt caacttgaag ggtatccaga tcaacgaccc gtccatcaac	720
agcgactcgg tcatgatgta ctccccggc gtccggcacc tgaaccacta caacaacatc	780
ttccagctaa actccacttt cctctctac atcaacgcca aagccgacaa gtgcggctac	840

aacgccttcc tcgacaaagc catcacctac ccacccccca gtcccttccc caccgcccct 900  
 gaaatcaccg aagactgcca agtctgggac gaagtcgtca tggccgccta cgacatcaac 960  
 ccttgcttca attactacca cctgatcgac ttctgcccct acctctggga cgtgctcggc 1020  
 ttccctctcc tcgctccgg cccaaacaac tacttcaacc gctccgacgt ccagaagatc 1080  
 ctgcacgtcc ctccaacgga ctactccgtg tgctcggaga ccgcatctt cgccaacggc 1140  
 gagggcagcg accccagctc ctgggggtccc ctaccagcg tcactgaacg cactaacaac 1200  
 actatcatcg gccacggctg gctcgattac ctctcttct tgaacggctc gctcgccaca 1260  
 atccagaaca tgacctgaa cggttaagcaa gggttccagc gtctcccggt ggaaccgctc 1320  
 ttctgcccct accattatgg tetggctgag ctgtactggg gcgatgagcc tgacccgat 1380  
 aaccttgatg ctggcgctgg atacctgggt acagcgcata ccgagcgagg gttgacttcc 1440  
 agctcggtgt atttgtctg tcataaaaac ccgcagtatg ttcttggtgc ggcttaccgc 1500  
 cagttggagt tctgctcgg taggattagt agtcttctcg cgaaggggaa ctatacctct 1560  
 tga 1563

<210> 3  
 <211> 520  
 <212> PRT  
 <213> *Aspergillus niger*

<400> 3

Met Arg Val Thr Thr Ala Ile Ala Ser Leu Leu Val Gly Ser Ala  
 1 5 10 15

Thr Ser Leu Gln Asn Pro His Arg Arg Ala Val Pro Pro Pro Leu Ser  
 20 25 30

His Arg Ser Val Ala Ser Arg Ser Val Pro Val Glu Arg Arg Thr Thr  
 35 40 45

Asp Phe Glu Tyr Leu Thr Asn Lys Thr Ala Arg Phe Leu Val Asn Gly  
 50 55 60

Thr Ser Ile Pro Glu Val Asp Phe Asp Val Gly Glu Ser Tyr Ala Gly  
 65 70 75 80

Leu Leu Pro Asn Thr Pro Thr Gly Asn Ser Ser Leu Phe Phe Trp Phe  
 85 90 95

Phe Pro Ser Gln Asn Pro Glu Ala Ser Asp Glu Ile Thr Ile Trp Leu  
100 105 110

Asn Gly Gly Pro Gly Cys Ser Ser Leu Asp Gly Leu Leu Gln Glu Asn  
115 120 125

Gly Pro Phe Leu Trp Gln Pro Gly Thr Tyr Lys Pro Val Pro Asn Pro  
130 135 140

Tyr Ser Trp Thr Asn Leu Thr Asn Val Val Tyr Ile Asp Gln Pro Ala  
145 150 155 160

Gly Thr Gly Phe Ser Pro Gly Pro Ser Thr Val Asn Asn Glu Glu Asp  
165 170 175

Val Ala Ala Gln Phe Asn Ser Trp Phe Lys His Phe Val Asp Thr Phe  
180 185 190

Asp Leu His Gly Arg Lys Val Tyr Ile Thr Gly Glu Ser Tyr Ala Gly  
195 200 205

Met Tyr Val Pro Tyr Ile Ala Asp Ala Met Leu Asn Glu Glu Asp Thr  
210 215 220

Thr Tyr Phe Asn Leu Lys Gly Ile Gln Ile Asn Asp Pro Ser Ile Asn  
225 230 235 240

Ser Asp Ser Val Met Met Tyr Ser Pro Ala Val Arg His Leu Asn His  
245 250 255

Tyr Asn Asn Ile Phe Gln Leu Asn Ser Thr Phe Leu Ser Tyr Ile Asn  
260 265 270

Ala Lys Ala Asp Lys Cys Gly Tyr Asn Ala Phe Leu Asp Lys Ala Ile  
275 280 285

Thr Tyr Pro Pro Pro Ser Pro Phe Pro Thr Ala Pro Glu Ile Thr Glu  
290 295 300

Asp Cys Gln Val Trp Asp Glu Val Val Met Ala Ala Tyr Asp Ile Asn  
305 310 315 320

Pro Cys Phe Asn Tyr Tyr His Leu Ile Asp Phe Cys Pro Tyr Leu Trp  
325 330 335

Asp Val Leu Gly Phe Pro Ser Leu Ala Ser Gly Pro Asn Asn Tyr Phe  
340 345 350

Asn Arg Ser Asp Val Gln Lys Ile Leu His Val Pro Pro Thr Asp Tyr  
355 360 365

Ser Val Cys Ser Glu Thr Val Ile Phe Ala Asn Gly Asp Gly Ser Asp  
370 375 380

Pro Ser Ser Trp Gly Pro Leu Pro Ser Val Ile Glu Arg Thr Asn Asn  
385 390 395 400

Thr Ile Ile Gly His Gly Trp Leu Asp Tyr Leu Leu Phe Leu Asn Gly  
405 410 415

Ser Leu Ala Thr Ile Gln Asn Met Thr Trp Asn Gly Lys Gln Gly Phe  
420 425 430

Gln Arg Pro Pro Val Glu Pro Leu Phe Val Pro Tyr His Tyr Gly Leu  
435 440 445

Ala Glu Leu Tyr Trp Gly Asp Glu Pro Asp Pro Tyr Asn Leu Asp Ala  
450 455 460

Gly Ala Gly Tyr Leu Gly Thr Ala His Thr Glu Arg Gly Leu Thr Phe  
465 470 475 480

Ser Ser Val Tyr Leu Ser Gly His Glu Ile Pro Gln Tyr Val Pro Gly  
485 490 495

Ala Ala Tyr Arg Gln Leu Glu Phe Leu Leu Gly Arg Ile Ser Ser Leu  
500 505 510

Ser Ala Lys Gly Asn Tyr Thr Ser  
515 520